Amendments to the Claims:

The listing of claims will replace all prior versions, and listings, of claims in the application. Material inserted is indicated by underlining and material deleted is indicated by ~~strikeout~~.

Listing of Claims:

1. (Original) Nucleic acid coding for a deletion variant of an urokinase receptor (uPAR), wherein the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, with the exception of GenBank sequence U 08839.

2. (Original) Nucleic acid according to claim 1, wherein the sequence of exon 4 and/or 5 is essentially missing fully.

3. (Currently amended) Nucleic acid according to claim 1 ~~or 2~~, wherein it codes for a deletion variant of human uPAR.

4. (Currently amended) Nucleic acid according to claim 1 ~~any one of claims 1 to 3~~, wherein it codes for a tumor associated uPAR variant.

5. (Currently amended) uPAR specific oligonucleotide, wherein it selectively hybridises with an uPAR deletion variant coding nucleic acid according to claim 1 ~~any one of claims 1 to 4~~.

6. (Original) uPAR specific oligonucleotide according to claim 5, wherein it spans the deletion region.

7. (Currently amended) Recombinant vector operatively linked with an expression control sequence and at least one copy of a nucleic acid according to claim 1 ~~any one of claims 1 to 4~~.

8. (Currently amended) Cell transformed by a nucleic acid according to claim 1 ~~any one of claims 1 to 4~~ or by a recombinant vector operatively linked with an expression control sequence and at least one copy of the nucleic acid ~~a recombinant vector according to claim 7~~.

9. (Currently amended) Method for the recombinant production of polypeptides comprising the steps of:
   (a) providing a nucleic acid according to claim 1 ~~any one of claims 1 to 4~~ or by a recombinant vector operatively linked with an expression control sequence and at least one copy of the nucleic acid ~~a vector according to claim 7~~.
   (b) introducing the nucleic acid or vector into a suitable host cell,
   (c) culturing the host cell in a suitable medium for the purpose of polypeptide expression, and
   (d) isolation of the expression product from the medium and/or the host cell.

10. (Original) Method according to claim 9, wherein the host cell is a mammalian cell, e.g. CHO.

11. (Currently amended) uPAR deletion variant coded by a nucleic acid according to claim 1 ~~any one of claims 1 to 4~~.

12. (Original) uPAR deletion variant according to claim 11, wherein it is tumor selectively expressed.

13. (Original) A fragment of an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, wherein it

displays a length of 6 to 50 amino acids and an uPAR deletion region characteristic amino acid sequence different from the native uPAR amino acid sequence.

14. (Original) Fragment according to claim 13, wherein it possesses an uPAR deletion variant characteristic antigenic epitope.

15. (Original) Use of an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, or fragments thereof, as immunogen for the production of antibodies.

16. (Original) Antibody against an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, wherein it displays essentially no cross reactivity against native uPAR.

17. (Original) Antibody according to claim 16, wherein it is conjugated with a marker group and/or cytotoxic group.

18. (Original) Antibody according to claim 17, wherein the cytotoxic group is selected from radionuclides and toxins.

19. (Original) Pharmaceutical composition, wherein the active component comprises:
    (a) a nucleic acid coding for an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, with the exception of GenBank sequence U08839,
    (b) a vector containing a nucleic acid according to (a),
    (c) a cell, containing a nucleic acid according to (a) or a vector according to (b),
    (d) an uPAR deletion variant, in which one or two exons are missing at least partially, or an antigenic fragment thereof, and/or

(e) an antibody directed against an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, or an antigenic fragment thereof.

20. (Original) Pharmaceutical composition for pharmaceutical use, wherein the active component comprises:

(a) a nucleic acid coding for an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, with the exception of GenBank sequence U08839,
(b) a vector containing a nucleic acid according to (a),
(c) a cell, containing a nucleic acid according to (a) or a vector according to (b),
(d) an uPAR deletion variant, in which one or two exons are missing at least partially, or an antigenic fragment thereof, and/or
(e) an antibody directed against an uPAR deletion variant, in which the sequence of exon 4 and/or exon 5 of the native sequence is at least partially missing, or an antigenic fragment thereof.

21. (Currently amended) Pharmaceutical composition according to claim 19 ~~or 20~~, wherein it further contains common pharmaceutical carriers, auxiliary agents and diluents.

22. (Currently amended) Pharmaceutical composition according to claim 19 ~~any one of claims 19 to 21~~ as diagnostic or therapeutic agent, wherein the uPAR deletion variant is del4, del5 or del4+5.

23. (Currently amended) Pharmaceutical composition, preferably comprising an antibody, according to claim 19 ~~or 20~~ as diagnostic agent for the prognosis of the course of tumor disease, wherein the uPAR deletion variant is del4, del5 or del4+5.

24. (Currently amended) Pharmaceutical composition, preferably comprising an antibody, according to claim 19 ~~or 20~~ for the detection of tumor cells in biological samples, wherein the uPAR deletion variant is del4, del5 or del4+5.

25. (Original) Pharmaceutical composition according to claim 23 as a therapeutic agent for the treatment of tumor disease.

26. (Currently amended) Pharmaceutical composition according to claim 23 ~~any one of claims 23 to 25~~ for breast and ovarian carcinoma´s.

27. (Currently amended) Pharmaceutical composition according to claim 22 ~~claim 22 or 23~~ as a cytostatic or cytotoxin of tumor cells.

28. (Currently amended) Pharmaceutical composition according to claim 22 ~~any one of claims 22 to 27~~, wherein the active component is an antibody directed against uPAR deletion variants del4, del5 and/or del4+5.

29. (Currently amended) Antibody according to claim 16 ~~any one of claims 16 to 18~~ directed against the uPAR deletion variants del4, del5 and/or del4+5 for the selective detection of uPAR deletion variants in biological samples comprising the steps of:

(a) providing a sample,
(b) contacting the sample with an antibody, and
(c) detecting the antibody binding to the sample.

30. (Original) Antibody according to claim 29, wherein the detection is done by ELISA.

31. (Currently amended) Antibody according to claim 29 ~~or 30~~, wherein a tumor sample is used, preferably isolated from mammary or ovarian carcinoma tissue.

32. (Original) Oligonucleotide according to claim 5 for the selective suppression of uPAR deletion variant expression.

33. (Original) Oligonucleotide according to claim 32, wherein the oligonucleotide spans the fusion region of one or more uPAR deletion variants.

34. (Currently amended) Oligonucleotide according to claim 32 ~~or 33~~, wherein the oligonucleotide selectively blocks the expression of uPAR deletion variants del4 and/or del5 and/or del4+5 at least partially.

35. (Original) Oligonucleotide according to claim 34, wherein a mixture of oligonucleotides are employed to block the expression of all uPAR variants del4, del5 and del4+5.

36. (Currently amended) Antibody according to claim 16 ~~any one of claims 16 to 18~~ as inhibitor of uPAR deletion variant activity.

37. (Currently amended) Antibody according to claim 16 ~~any one of claims 16 to 18~~ directed against the uPAR deletion variants del4, del5 and del4+5 as molecular detection systems for the detection of uPAR deletion variants in biological samples.

38. (Original) Use of an uPAR deletion variant, in which the sequences of exon 4 and/or exon 5 of the native sequence is at least missing partially, or a coding nucleic acid thereof in a method useful for the identification of agents, that selectively modulate the activity of an uPAR deletion variant, especially inhibit the activity of an uPAR variant.

39. (Original) A method for the detection of tumors associated with the generation of at least one uPAR deletion variant comprising the steps of:

(a) obtaining a cDNA containing sample from a tumor to be investigated, and

(b) analysing the cDNA of said sample to determine whether alternative splicing of uPAR has occurred and at least one uPAR deletion variant has been generated, wherein the at least one uPAR deletion variant is del4, del5 and/or del4+5.

40. (Original) The method according to claim 39, wherein the step of analysing the cDNA of said sample comprises: amplifying the cDNA to obtain a quantified control amplification product comprising the nucleic acid coding for wild type uPAR or a fragment thereof and a quantified amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof, if present, and determining the ratio of wild type uPAR:uPAR deletion variant by comparing the quantified amplification products.

41. (Currently amended) The method according to claim 39 ~~or 40~~, wherein the cDNA is amplified with a first set of primers complementary to sequences contained in regions bridging the deleted sequences in uPAR deletion variants to obtain the amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof, and wherein the cDNA is amplified with a second set of primers complementary to sequences contained in the wild type uPAR to obtain the control amplification product comprising the nucleic acid coding for wild type uPAR or a fragment thereof.

42. (Currently amended) The method according to claim 39 ~~any one of claims 39 to 41~~, wherein the amplification of the cDNA is done by real-time RT-PCR amplification.

43. (Currently amended) The method according to claim 39 ~~any one of claims 39 to 42~~, wherein the amplification of the cDNA is done by real-time LC RT-PCR.

44. (Currently amended) The method according to claim 39 ~~any one of claims 39 to 43~~, wherein the tumor sample is obtained from a patient, e.g. a human being.

45. (Currently amended) The method according to claim 39 ~~any one of claims 39 to 44~~ for providing a prognosis for tumors associated with the generation of at least one uPAR deletion variant.

46. (Original) The method according to claim 45, wherein the ratio of wild type uPAR:uPAR deletion variant is greater than 0.043.

47. (Currently amended) The method according to claim 45 ~~or 46~~, wherein the tumors are selected from the group consisting of breast, ovarian, small cell lung, and pancreatic tumors.

48. (Currently amended) The method according to claim 45 ~~any one of claims 45 to 47~~, wherein the tumor is breast tumor.

49. (Currently amended) The method according to claim 45 ~~any one of claims 45 to 48~~, wherein the prognosis comprises the characterization of tumors associated with the generation of at least one uPAR deletion variant, e.g. if the tumors investigated are more invasive, are more likely to have metastasis, are more likely to have a shorter disease free survival period or have higher rates of recurrence than tumors not associated with the generation of uPAR deletion variants.

50. (Original) A method of predicting the risk of cancer in a tumor-bearing patient comprising the steps of:
(a) obtaining a cDNA containing sample from a tumor of said patient, and
(b) analysing the cDNA of said sample to determine whether alternative splicing of uPAR has occurred and at least one uPAR deletion variant has been generated, wherein the at least one uPAR deletion variant is del4, del5 and/or del4+5,

wherein patients having tumors associated with the generation of at least one uPAR deletion variant are at a higher risk to develop cancer than patients having tumors not associated with the generation of uPAR deletion variants.

51. (Original) The method according to claim 50, wherein the step of analysing the cDNA of said sample comprises: amplifying the cDNA to obtain a quantified amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof, if present.

52. (Currently amended) The method according to claim 50 ~~or 51~~, wherein the cDNA is amplified with a set of primers complementary to sequences contained in regions bridging the deleted sequences in uPAR deletion variants to obtain the amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof.

53. (Currently amended) The method according to claim 50 ~~any one of claims 50 to 52~~, wherein the amplification of the cDNA is done by real-time RT-PCR amplification.

54. (Currently amended) The method according to claim 50 ~~any one of claims 50 to 53~~, wherein the amplification of the cDNA is done by real-time LC RT-PCR.

55. (Currently amended) The method according to claim 50 ~~any one of claims 50 to 54~~, wherein the tumor is a breast, ovarian, small cell lung, or pancreatic tumor.

56. (Original) A method of providing a prognosis for a tumor-bearing patient comprising the steps of:

(a) obtaining a cDNA containing sample from a tumor of said patient,

(b) analysing the cDNA of said sample to determine whether alternative splicing of uPAR has occurred and at least one uPAR deletion variant has been generated, wherein the at least one uPAR deletion variant is del4, del5 and/or del4+5, and

(c) correlating the presence of the at least one uPAR deletion variant in the tumor of the patient with a prognosis of the patient.

57. (Original) The method according to claim 56, wherein the step of analysing the cDNA of said sample comprises: amplifying the cDNA to obtain a quantified control amplification product comprising the nucleic acid coding for wild type uPAR or a fragment thereof and a quantified amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof, if present, and determining the ratio of wild type uPAR:uPAR deletion variant by comparing the quantified amplification products.

58. (Currently amended) The method according to claim 56 ~~or 57~~, wherein the cDNA is amplified with a first set of primers complementary to sequences contained in regions bridging the deleted sequences in uPAR deletion variants to obtain the amplification product comprising the nucleic acid coding for the at least one uPAR deletion variant or a fragment thereof, and wherein the cDNA is amplified with a second set of primers complementary to sequences contained in the wild type uPAR to obtain the control amplification product comprising the nucleic acid coding for wild type uPAR or a fragment thereof.

59. (Currently amended) The method according to claim 56 ~~any one of claims 56 to 58~~, wherein the amplification of the cDNA is done by real-time RT-PCR amplification.

60. (Currently amended) The method according to claim 56 ~~any one of claims 56 to 59~~, wherein the amplification of the cDNA is done by real-time LC RT-PCR.

61. (Currently amended) The method according to claim 56 ~~any one of claims 56 to 60~~, wherein the tumor is a breast, ovarian, small cell lung, or pancreatic tumor.